MalE-CORE+1 RECOMBINANT PROTEINS

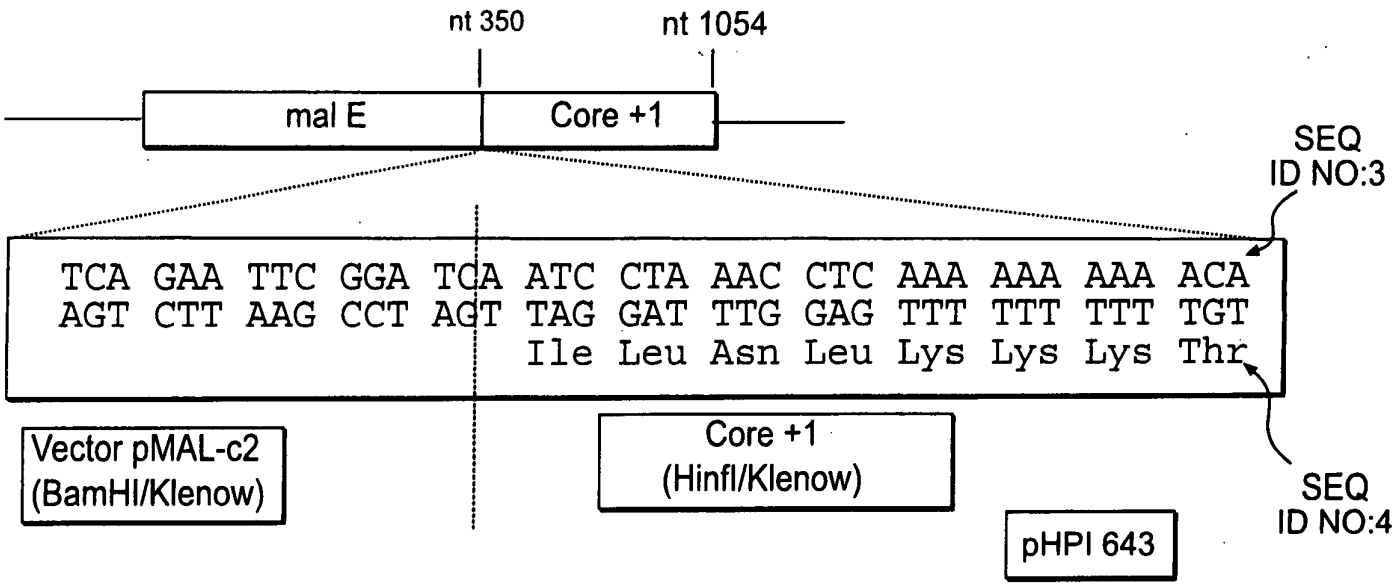



FIG. 1A



Substitute Figure

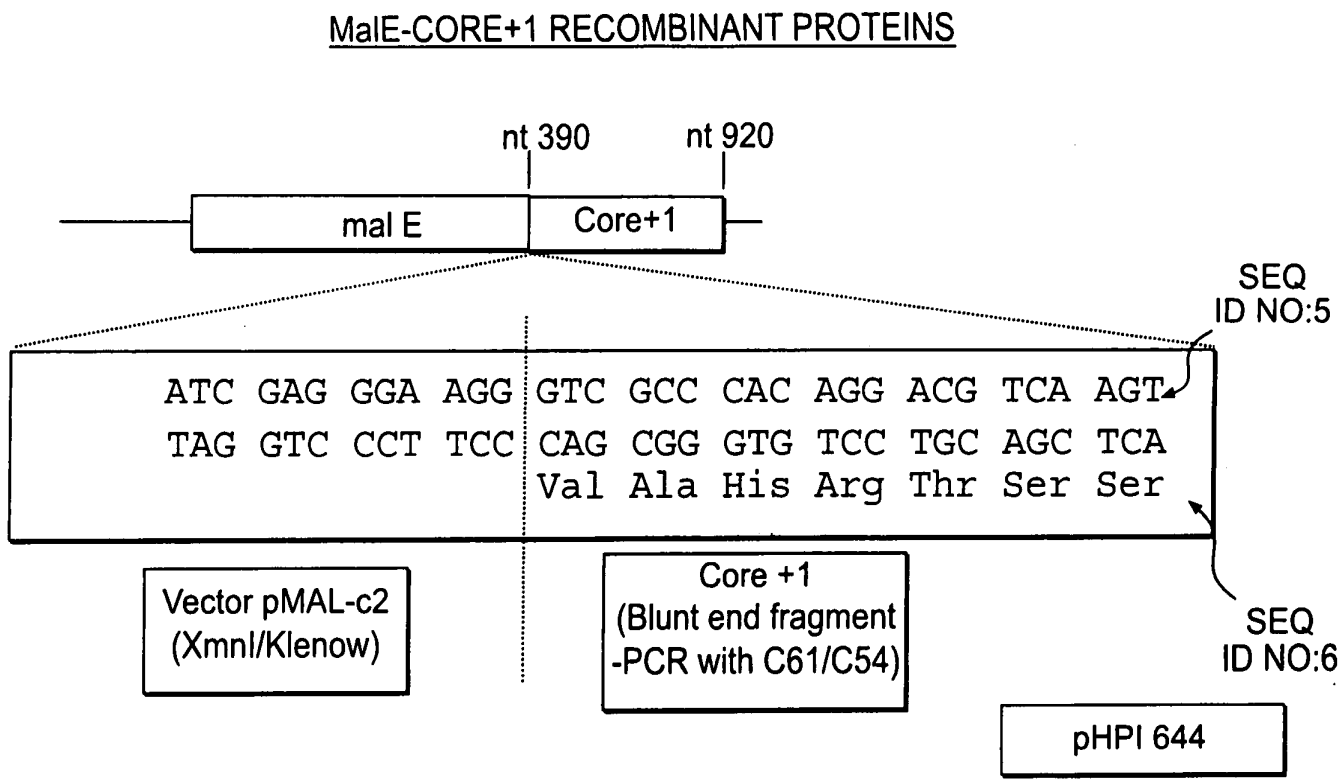



FIG. 1B

Substitute Figure

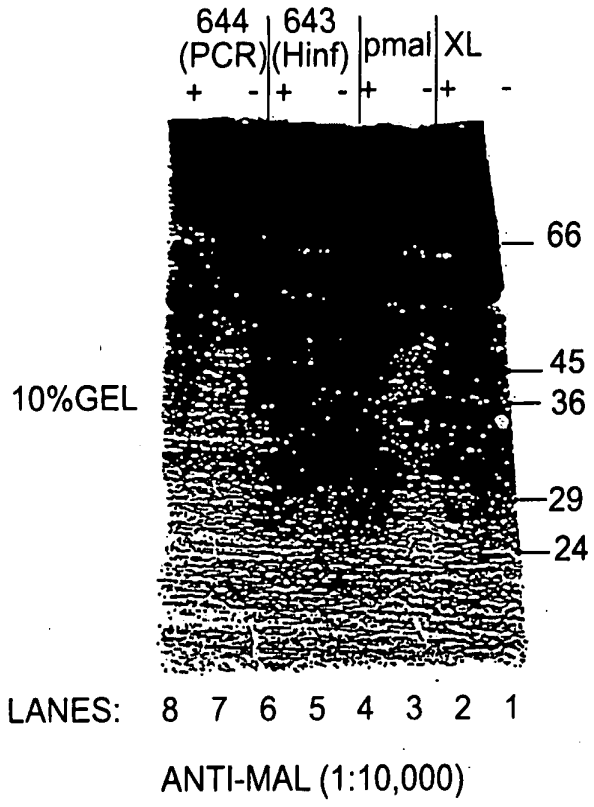



FIG. 2A

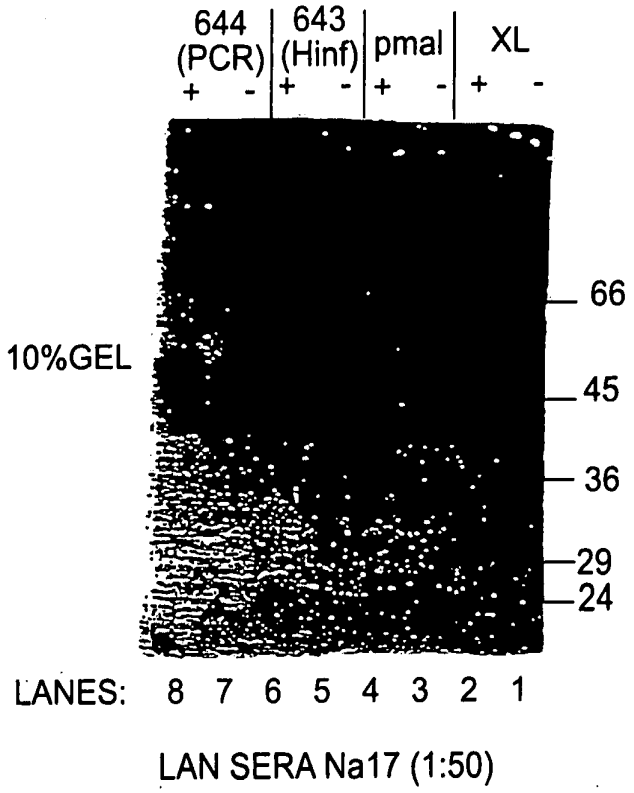



FIG. 2B

Substitute Figure

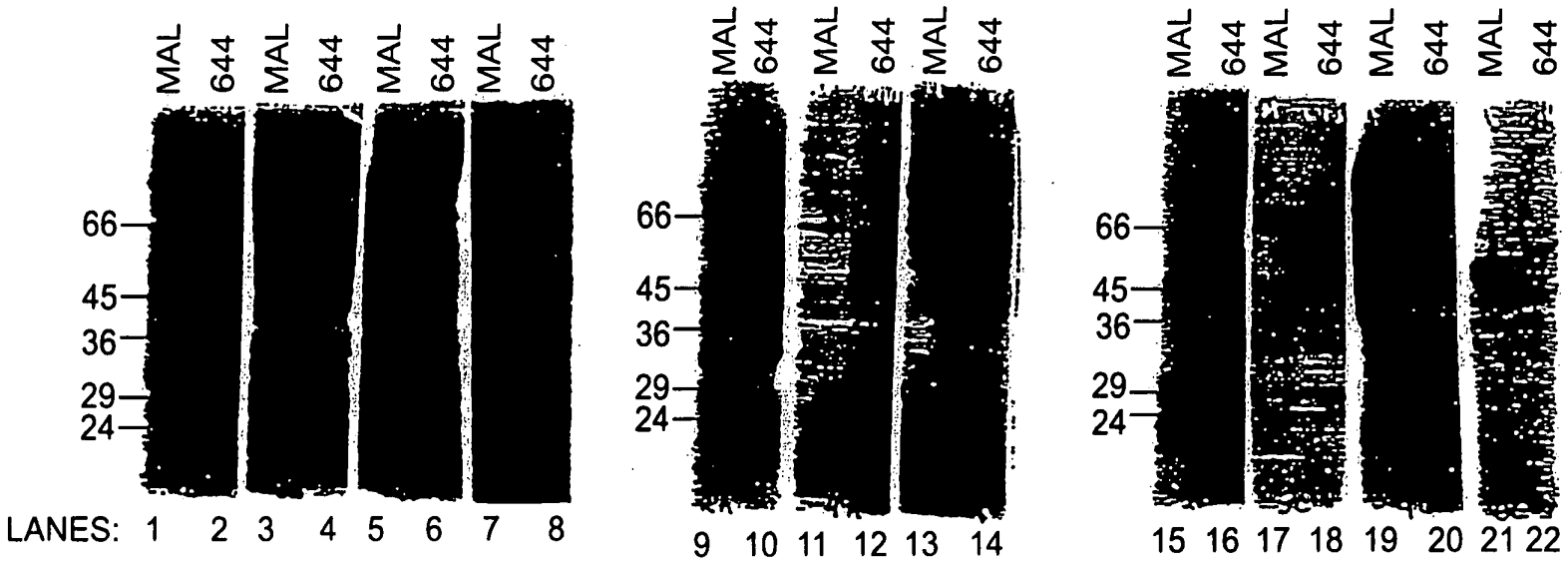



FIG. 3A

Substitute Figure

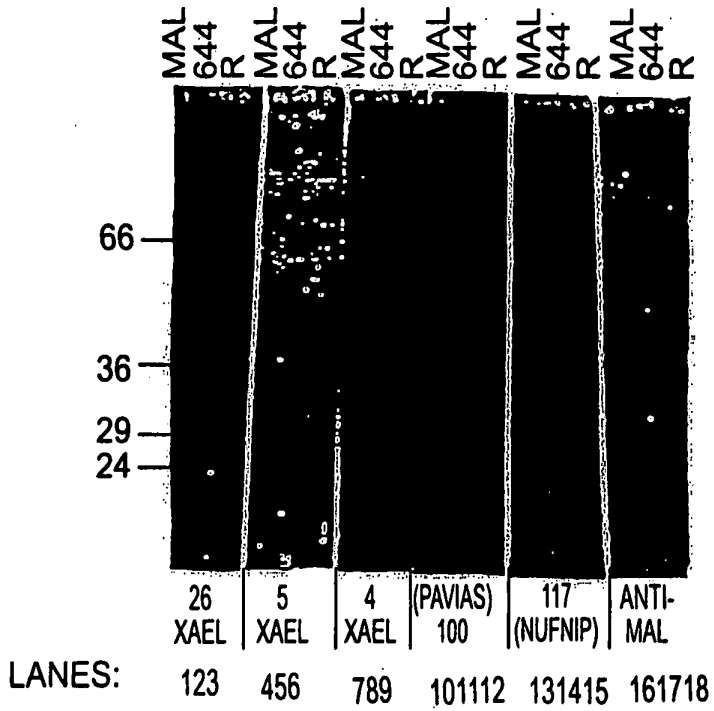



FIG. 3B

Substitute Figure

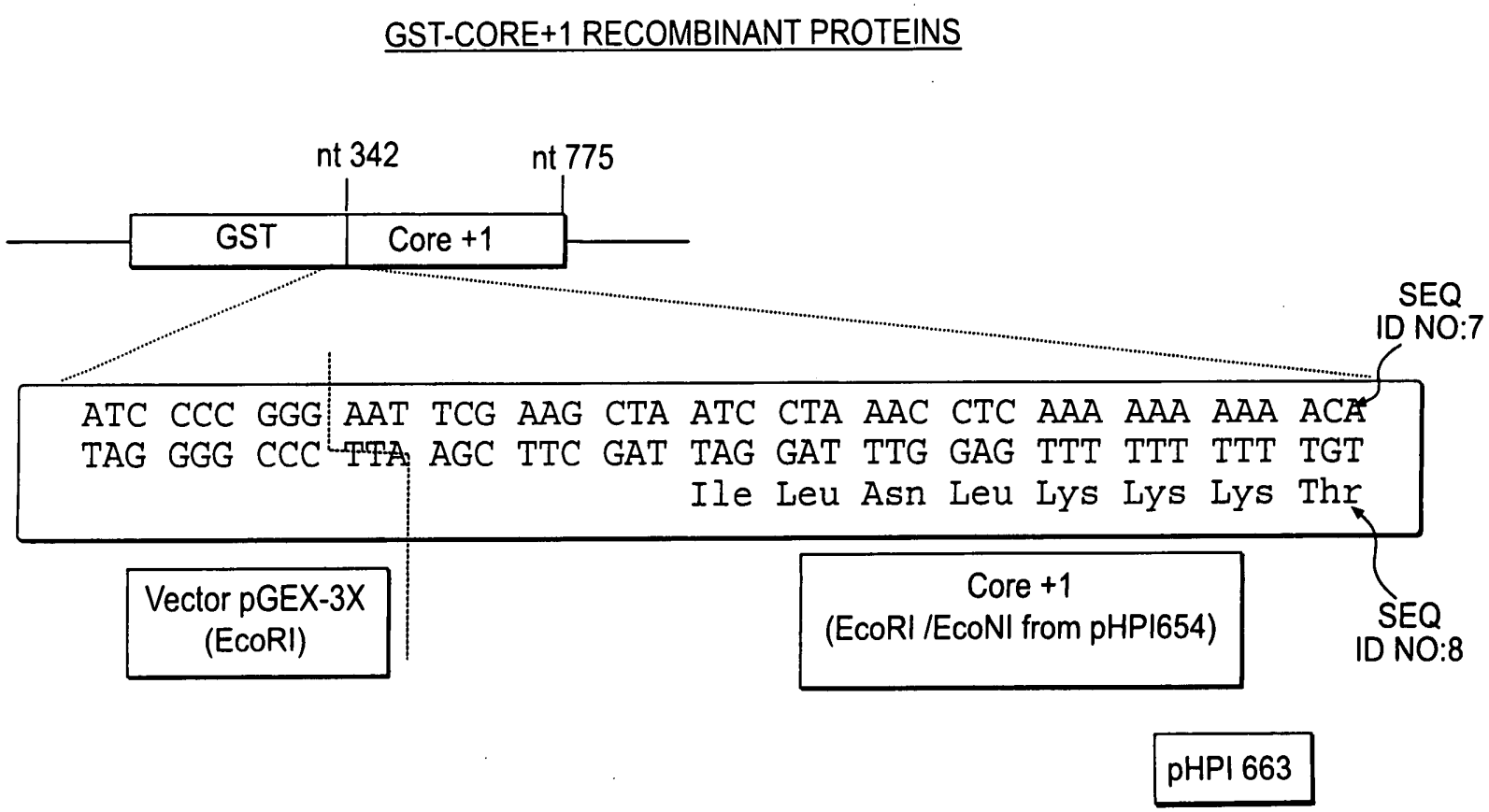

GST-CORE+1 RECOMBINANT PROTEINS
nt 342
nt 775
GST
Core +1
SEQ
ID NO:7
ATC CCC GGG AAT TCG AAG CTA ATC CTA AAC CTC AAA AAA AAA ACA
TAG GGG CCC TTA AGC TTC GAT TAG GAT TTG GAG TTT TTT TTT TGT
Ile Leu Asn Leu Lys Lys Lys Thr
Vector pGEX-3X
(EcoRI)
Core +1
(EcoRI /EcoNI from pHPI654)
SEQ
ID NO:8
pHPI 663

FIG. 4A

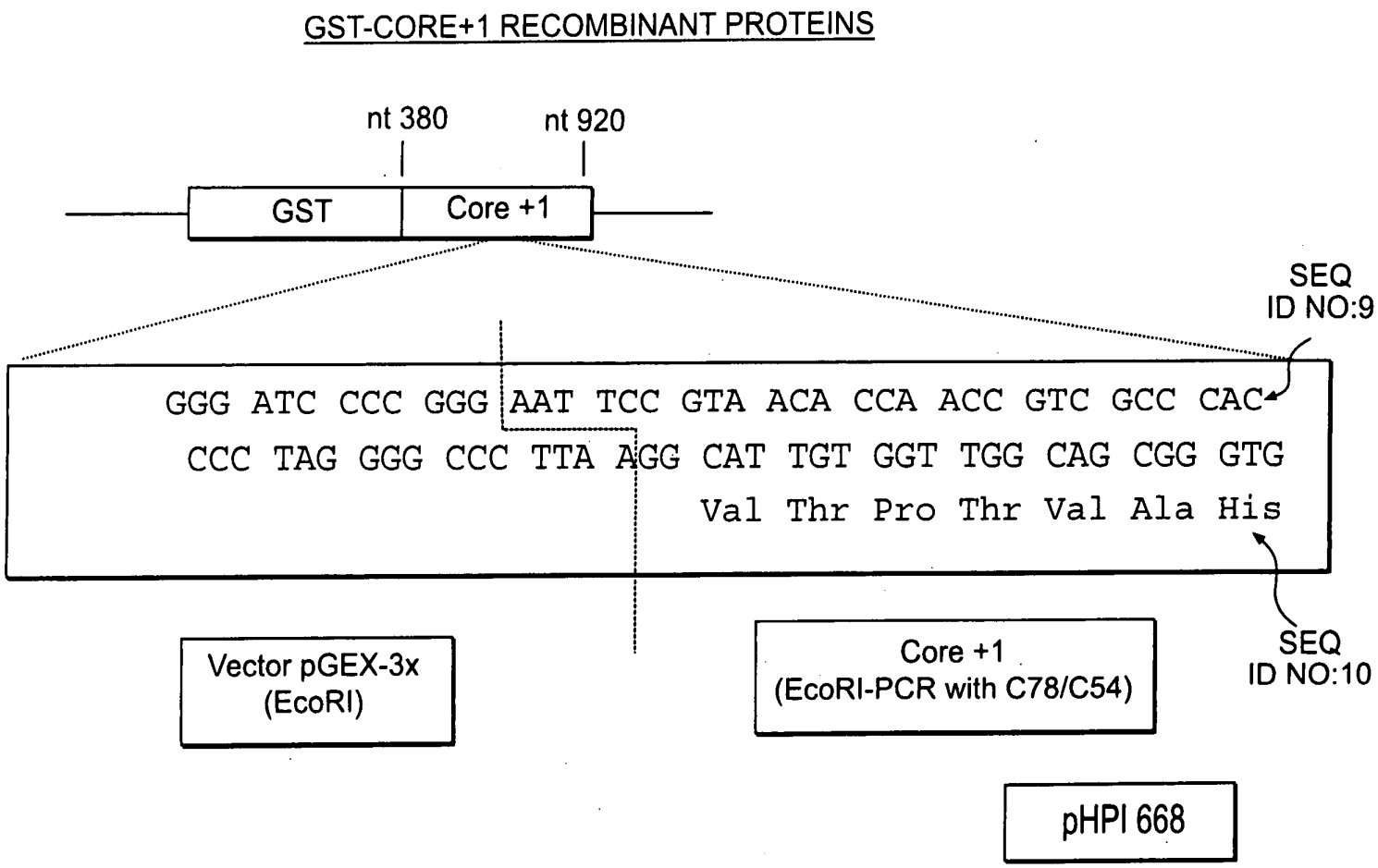

GST-CORE+1 RECOMBINANT PROTEINS
nt 380
nt 920
GST
Core +1
SEQ
ID NO:9
GGG ATC CCC GGG AAT TCC GTA ACA CCA ACC GTC GCC CAC
CCC TAG GGG CCC TTA AGG CAT TGT GGT TGG CAG CGG GTG
Val Thr Pro Thr Val Ala His
SEQ
ID NO:10
Vector pGEX-3x
(EcoRI)
Core +1
(EcoRI-PCR with C78/C54)
pHPI 668

***FIG. 4B***

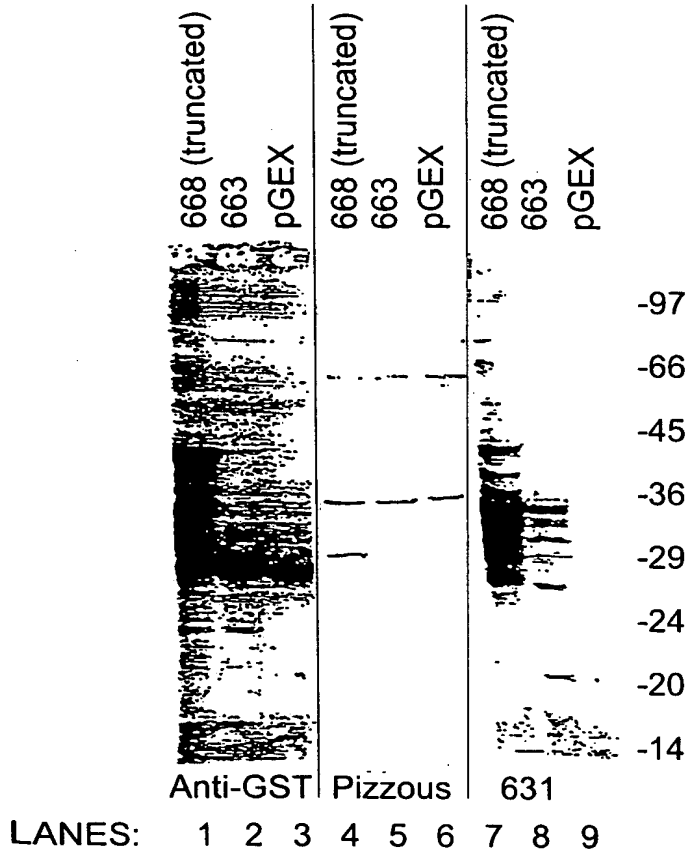



*FIG. 5*

Substitute Figure

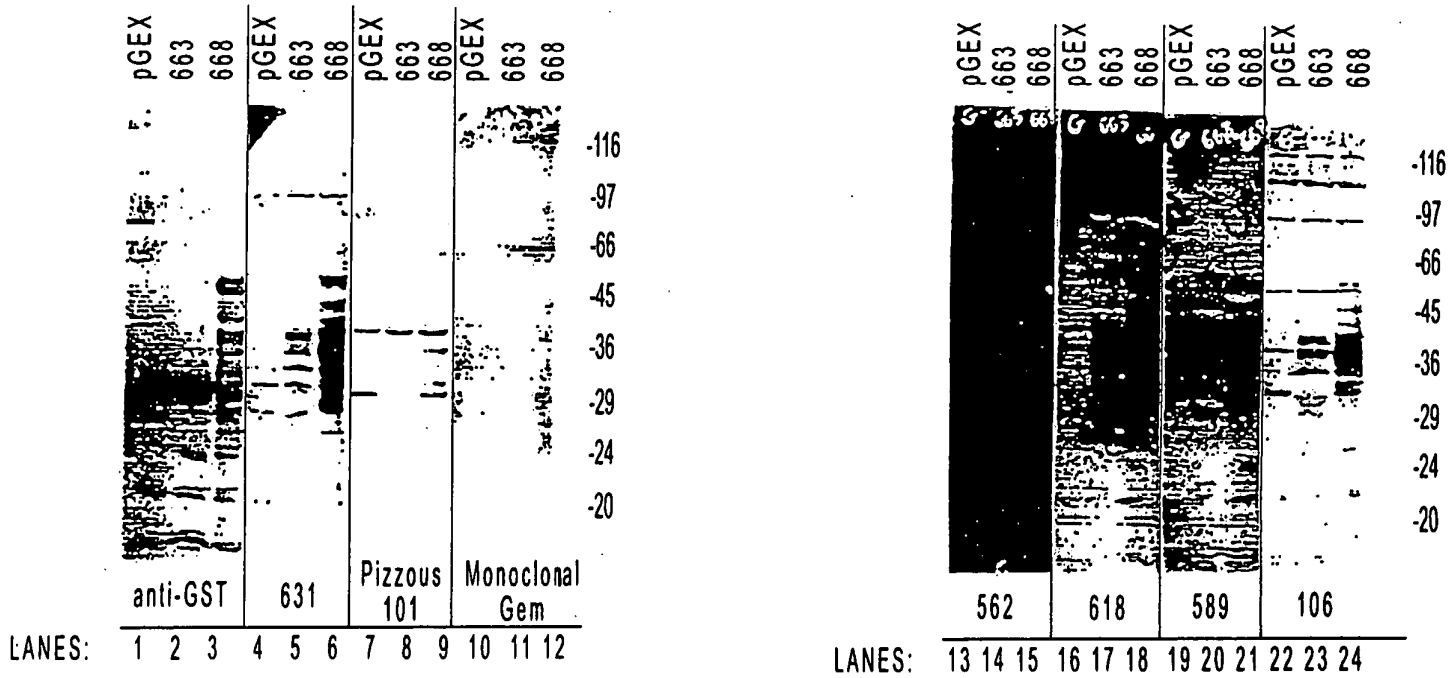



FIG. 6

Substitute Figure

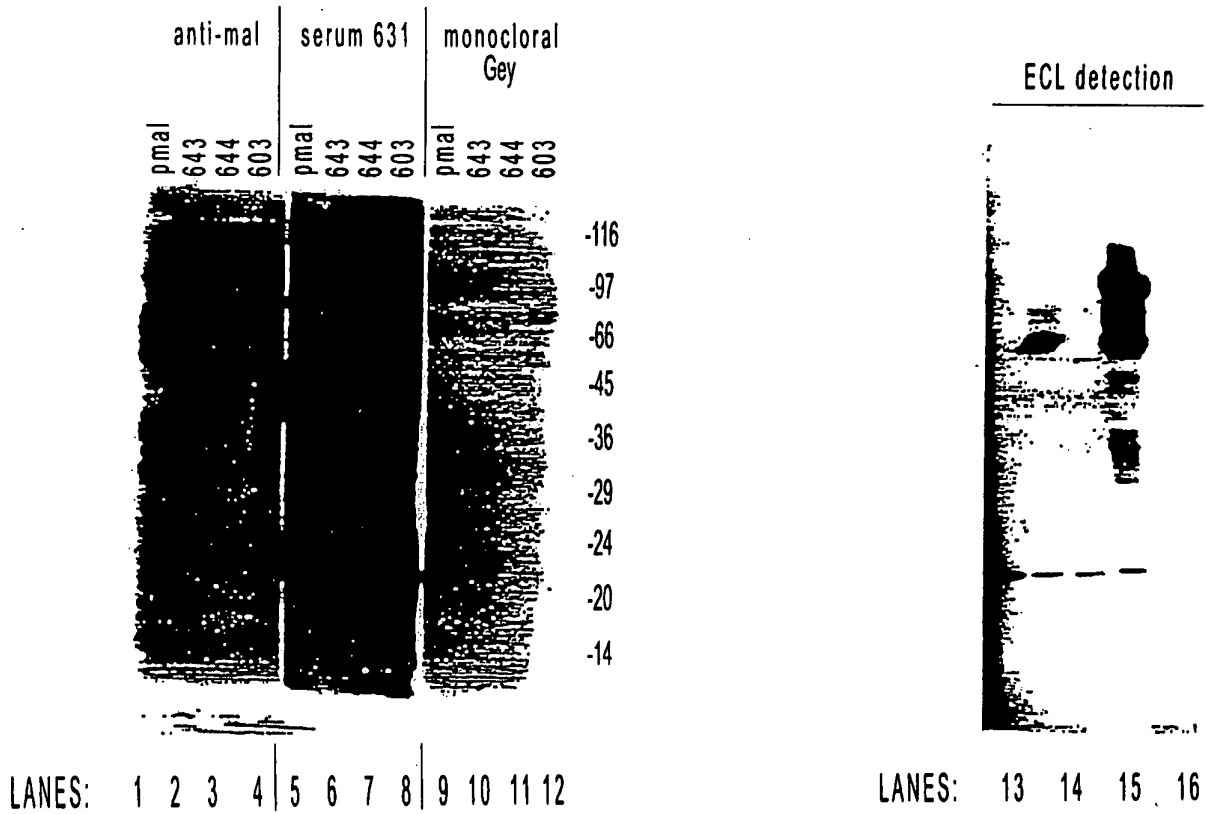



FIG. 7A

Substitute Figure

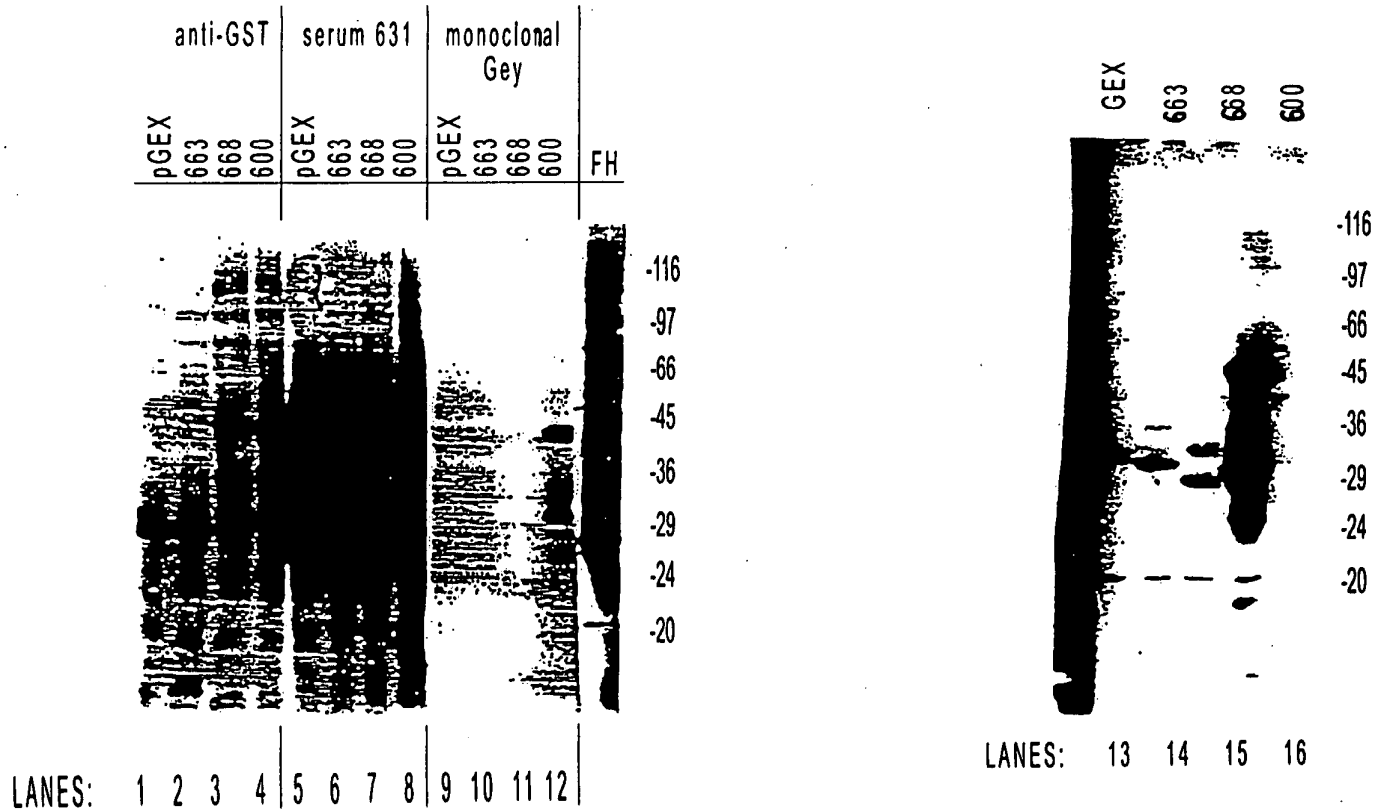



FIG. 7B

Substitute Figure

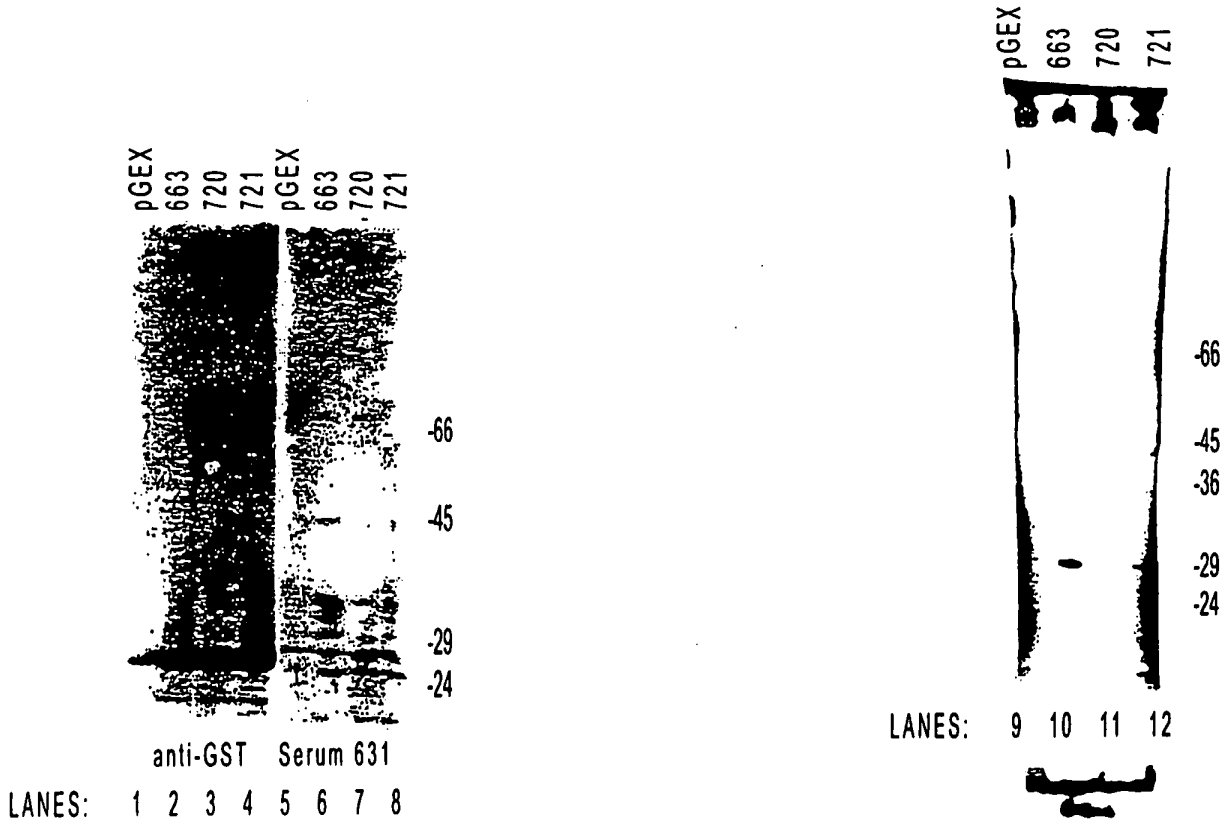



FIG. 8

Substitute Figure

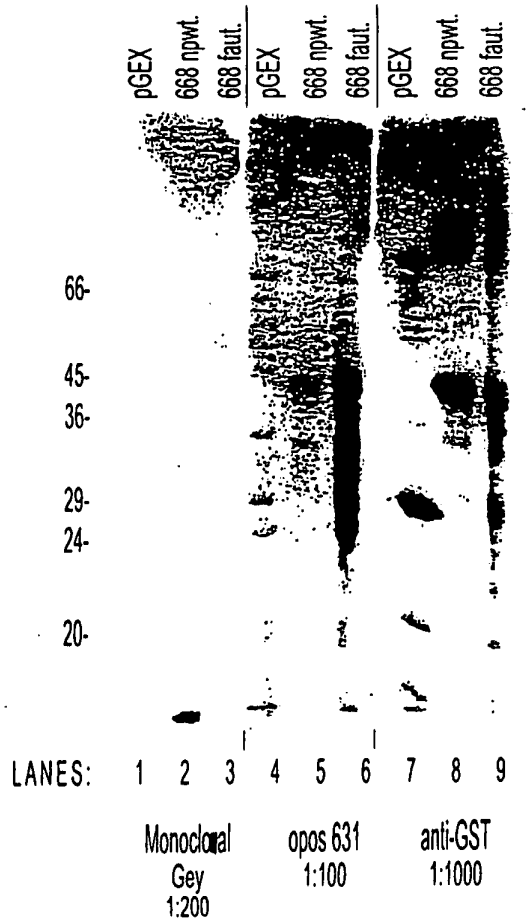



FIG. 9A

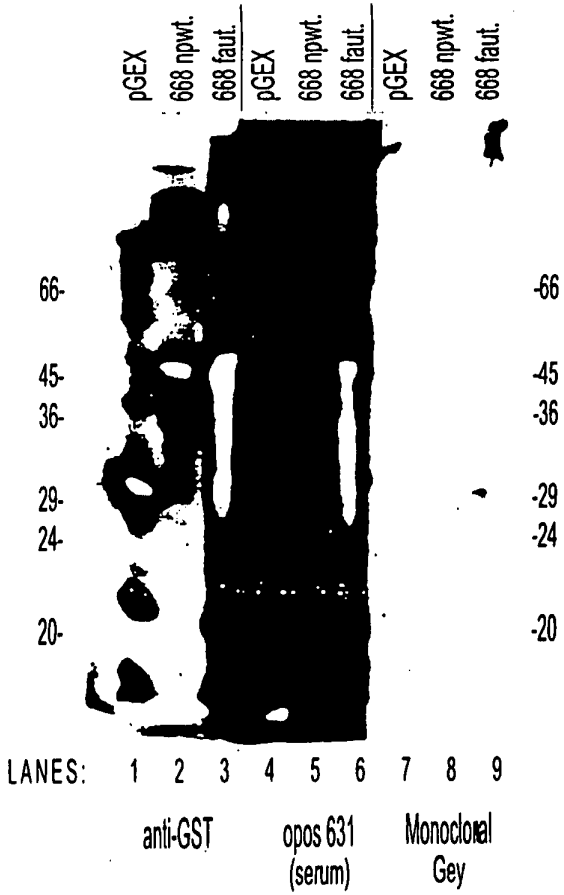



FIG. 9B

Substitute Figure

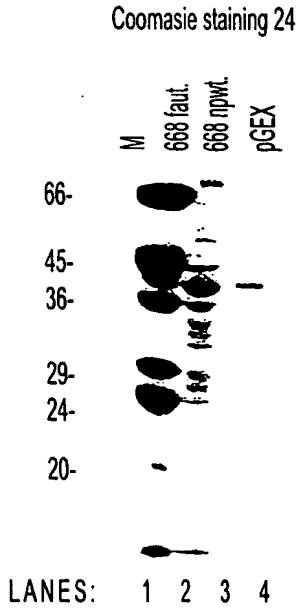
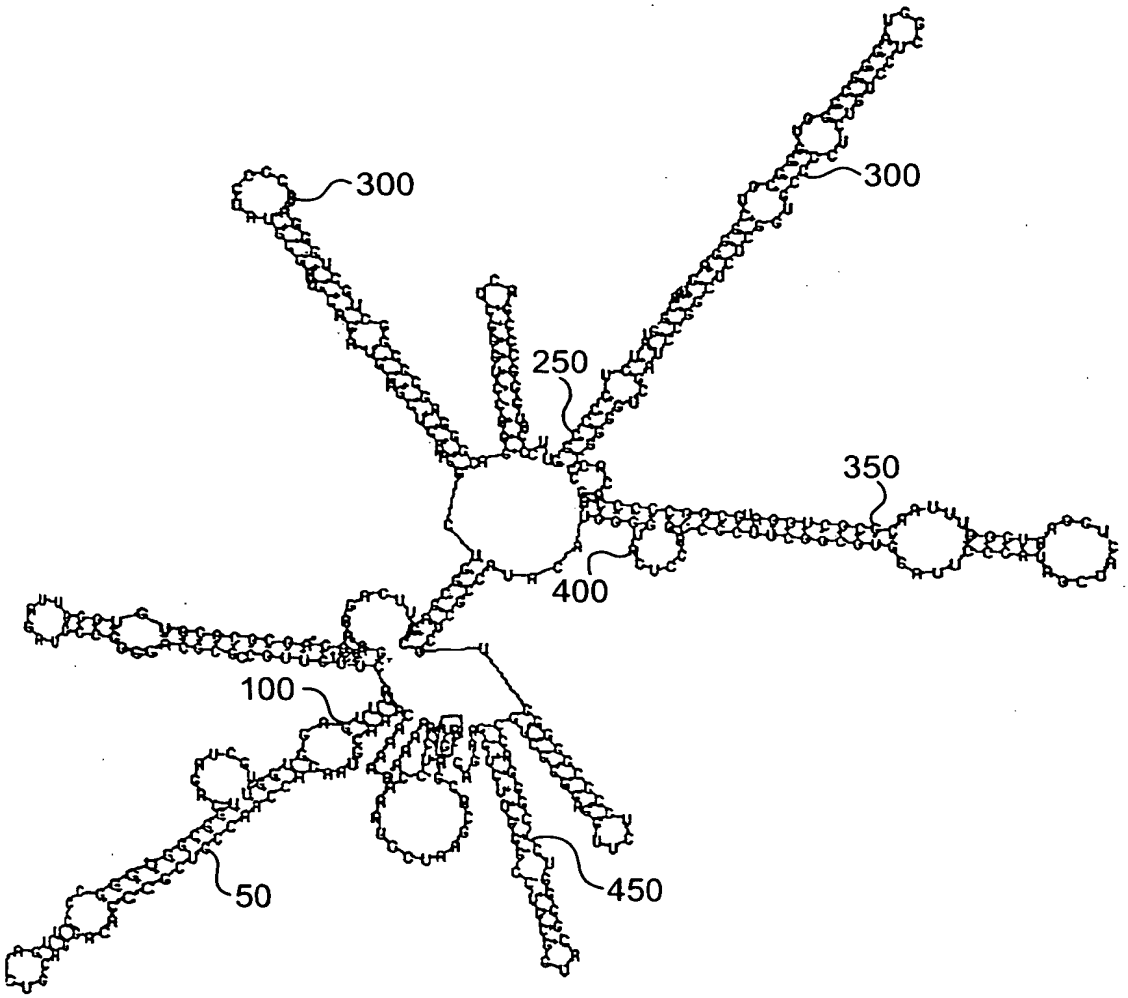

Coomasie staining 24
M
668 faut.
668 npwt.
pGEX
66-
45-
36-
29-
24-
20-
LANES: 1 2 3 4

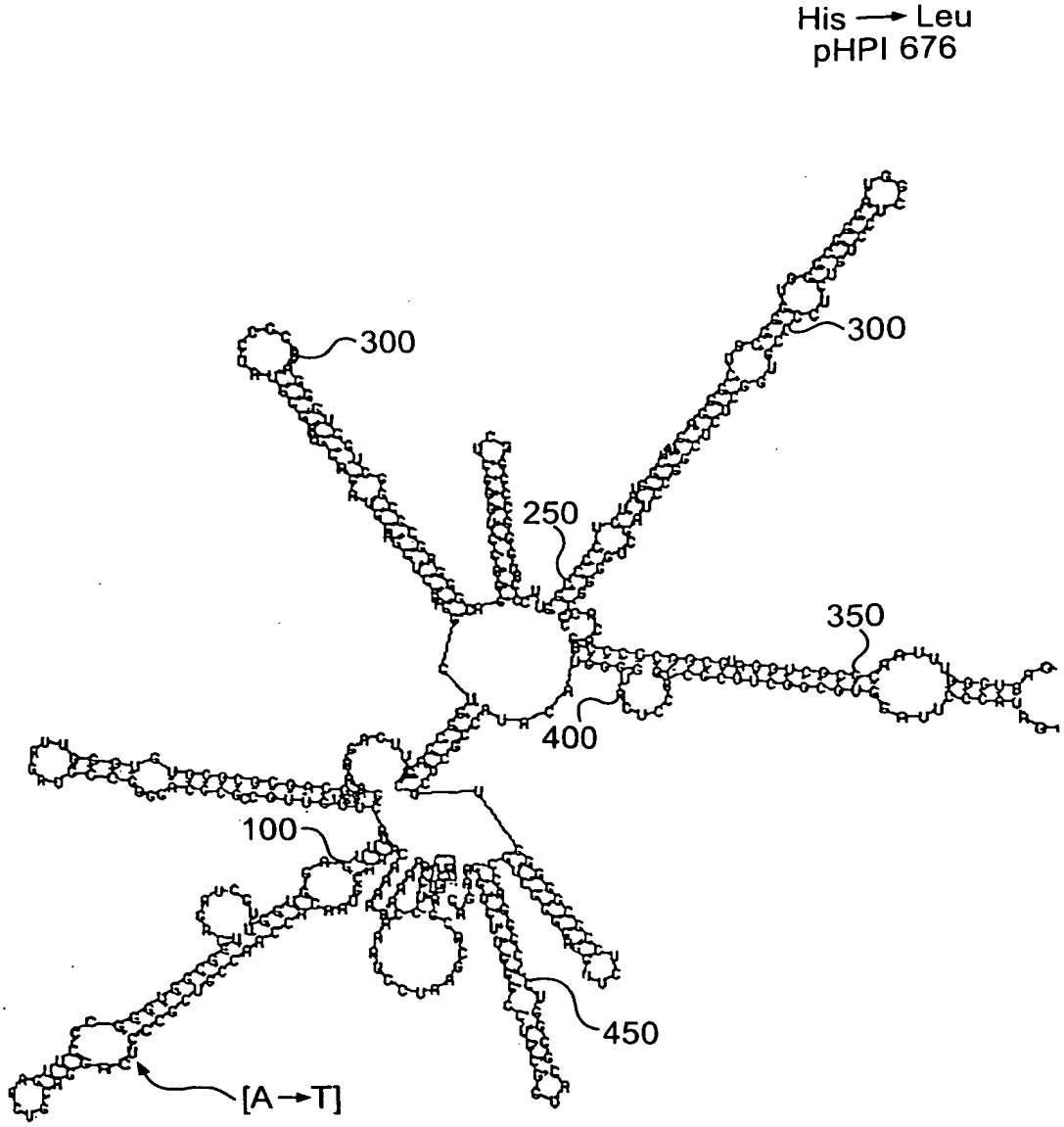
FIG. 9C

WILD TYPE
pHPI 643 & pHPI 663




(SEQ ID NO: 11)

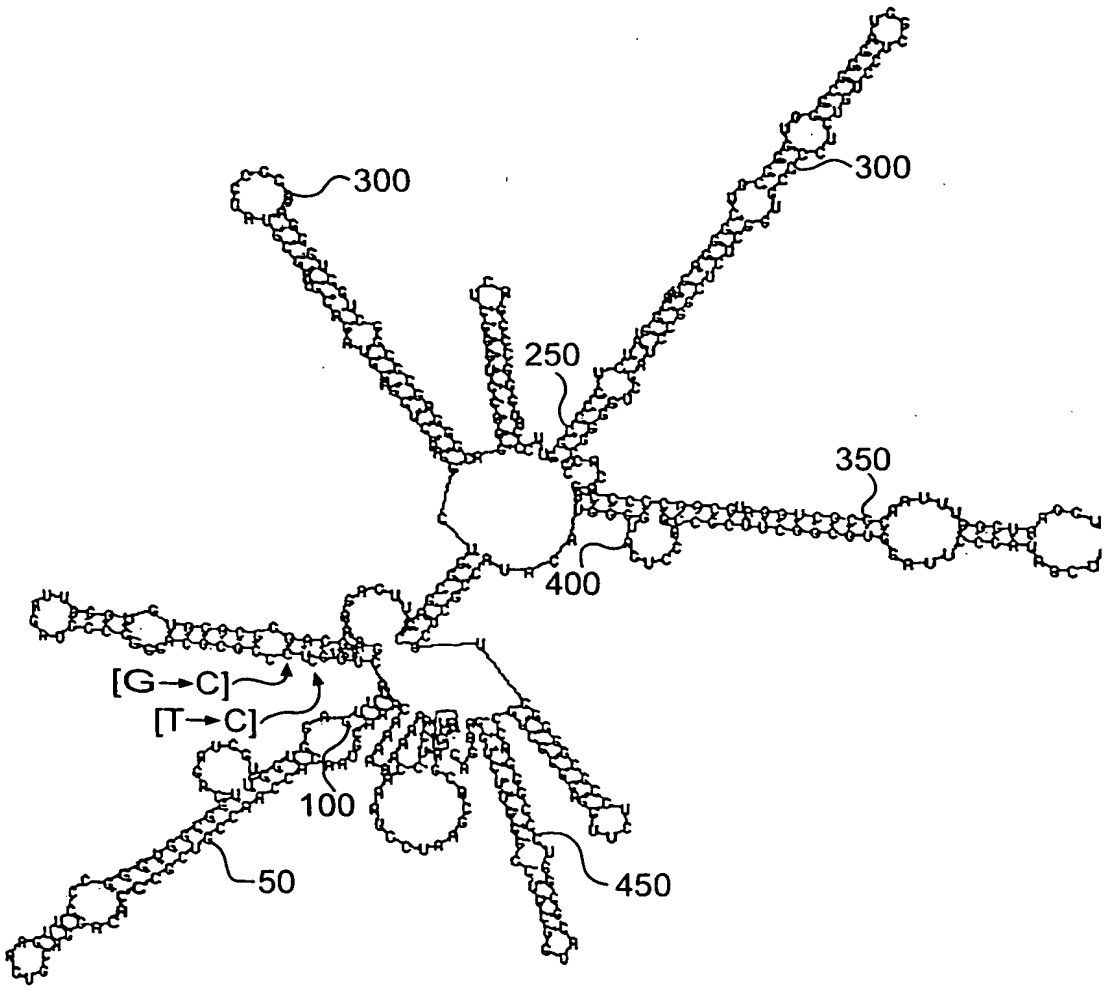
***FIG. 10A***




(SEQ ID NO: 12)

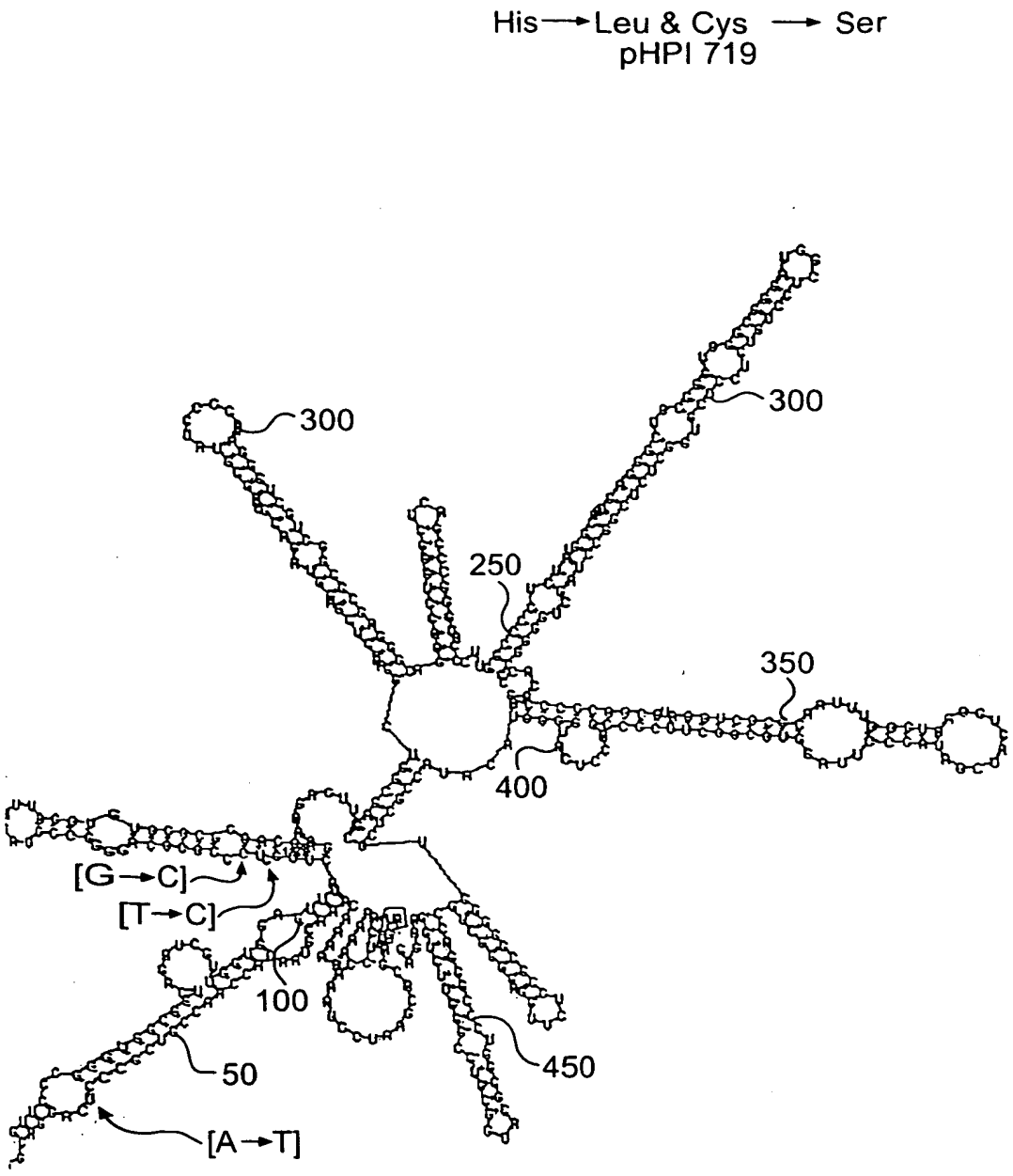
FIG. 10B

Cys → Ser
pHPI 679




(SEQ ID NO: 13)

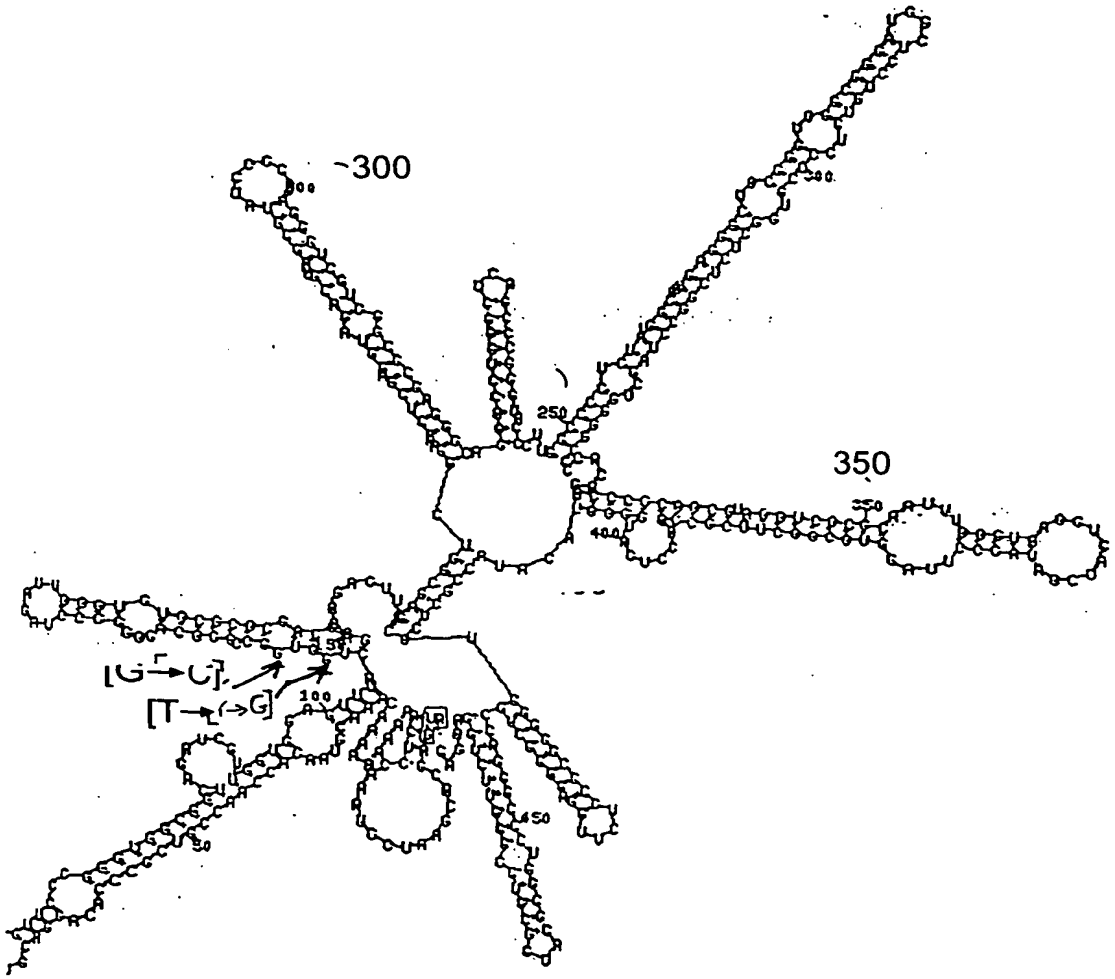
***FIG. 10C***




(SEQ ID NO: 14)

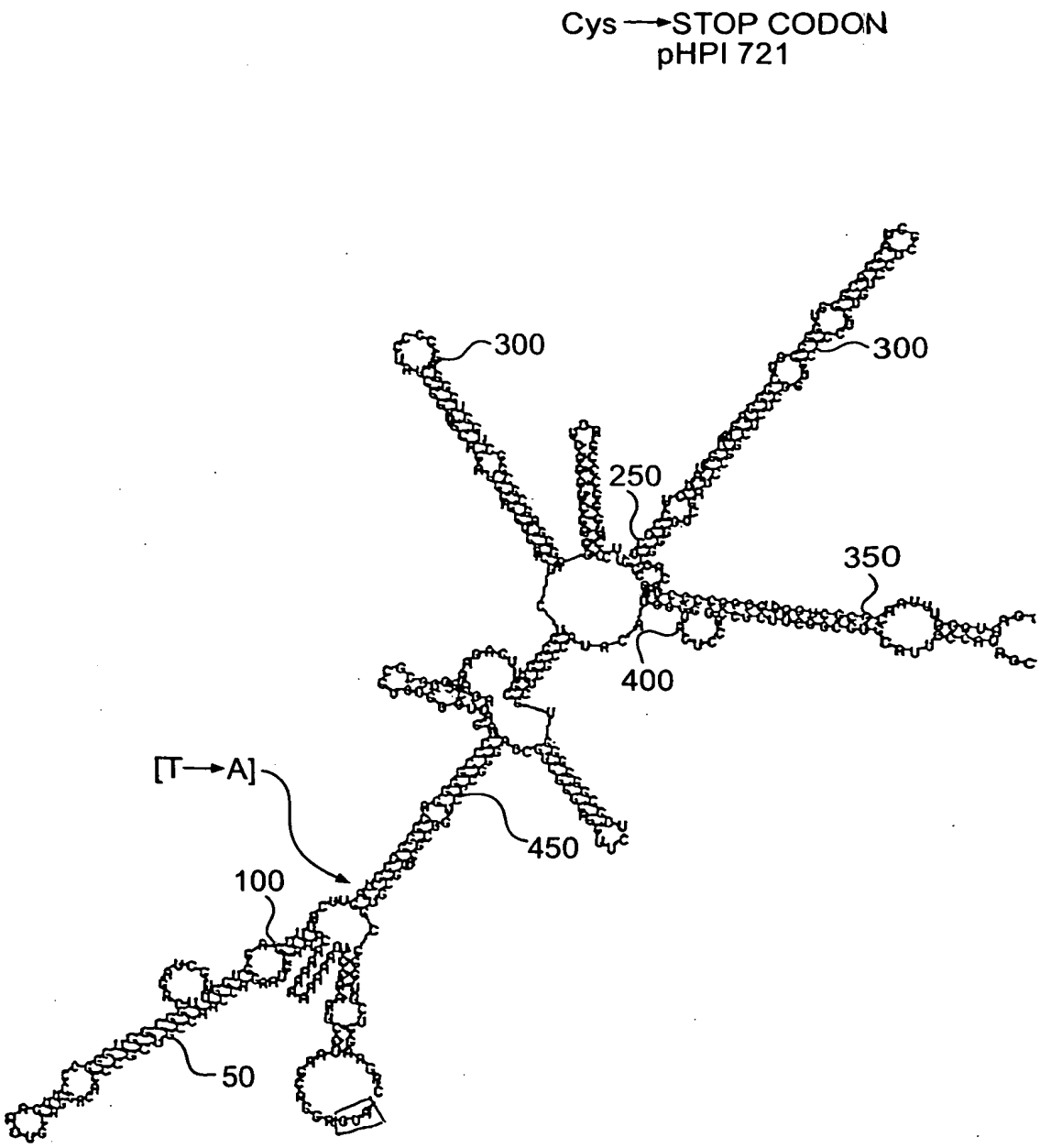
FIG. 10D

Cys-Cys → Gly- Gly
pHPI 720



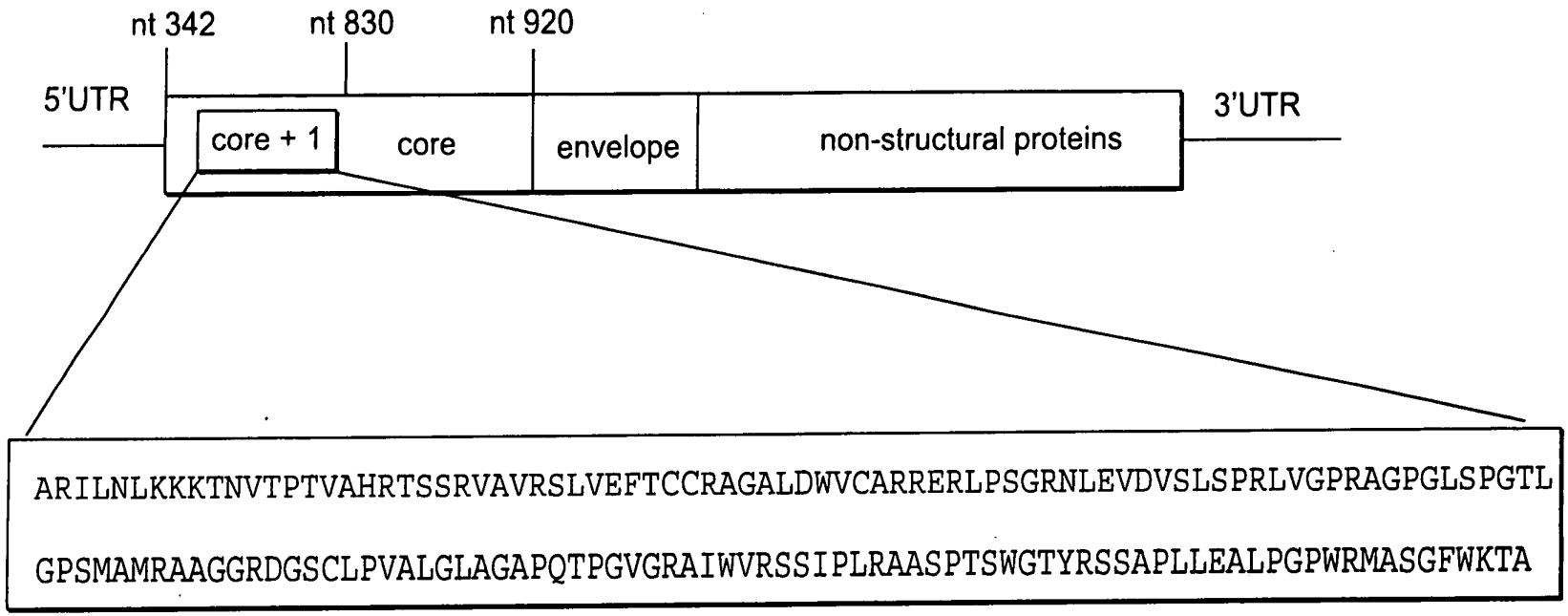

(SEQ ID NO: 15)

FIG. 10E




(SEQ ID NO: 16)

FIG. 10F




(amino acids 1 to 161 of SEQ ID NO:1)

FIG. 11

Substitute Figure

SEQUENCE RANGE: 342 TO 840

```
                350           360           370           380           390
                 *     *       *     *       *     *       *     *       *     *
(SEQ ID NO:2)A TGA GCA CGA ATC CTA AAC CTC AAA AAA AAA ACA AAC GTA ACA CCA ACC
(SEQ ID NO:1)T ACT CGT GCT TAG GAT TTG GAG TTT TTT TTT TGT TTG CAT TGT GGT TGG
               *** Ala Arg Ile Leu Asn Leu Lys Lys Lys Thr Asn Val Thr Pro Thr>
               ___a___a____TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a___a___a___>
```

PUTATIVE SLIPPERY SIGNAL

```
                400           410           420           430
                 *     *       *     *       *     *       *     *       *     *
               GTC GCC CAC AGG ACG TCA AGT TCC CGG GTG GCG GTC AGA TCG TTG GTG
               CAG CGG GTG TCC TGC AGT TCA AGG GCC CAC CGC CAG TCT AGC AAC CAC
               Val Ala His Arg Thr Ser Ser Ser Arg Val Ala Val Arg Ser Leu Val>
               ___a___a____TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a___a___a___>

          440           450           460           470           480
           *     *       *     *       *     *       *     *       *     *
          GAG TTT ACT TGT TGC CGC GCA GGG GCC CTA GAT TGG GTG TGC GCG CGA
          CTC AAA TGA ACA ACG GCG CGT CCC CGG GAT CTA ACC CAC ACG CGC GCT
          Glu Phe Thr Cys Cys Arg Ala Gly Ala Leu Asp Trp Val Cys Ala Arg>
          ___a___a____TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a___a___a___>
```

FIG. 12A

```
 490          500          510          520          530
   *     *      *      *     *      *     *     *      *
CGA GAA AGA CTT CCG AGC GGT CGC AAC CTC GAG GTA GAC GTC AGC CTA
GCT CTT TCT GAA GGC TCG CCA GCG TTG GAG CTC CAT CTG CAG TCG GAT
Arg Glu Arg Leu Pro Ser Gly Arg Asn Leu Glu Val Asp Val Ser Leu>
___a___a____TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a___a___a___>

    540          550          560          570          580
*     *      *      *     *      *     *     *      *      *
TCC CCA AGG CTC GTC GGC CCG AGG GCA GGA CCT GGG CTC AGC CCG GGT
AGG GGT TCC GAG CAG CCG GGC TCC CGT CCT GGA CCC GAG TCG GGC CCA
Ser Pro Arg Leu Val Gly Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly>
___a___a____TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a___a___a___>

      590          600          610          620          630
  *      *      *     *      *      *     *      *      *     *
ACC CTT GGC CCC TCT ATG GCA ATG AGG GCT GCG GGT GGG CGG GAT GGC
TGG GAA CCG GGG AGA TAC CGT TAC TCC CGA CGC CCA CCC GCC CTA CCG
Thr Leu Gly Pro Ser Met Ala Met Arg Ala Ala Gly Gly Arg Asp Gly
___a___a____TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a___a___a___>
```

FIG. 12B

```
          640          650          660          670
      *      *     *      *      *     *      *      *     *
TCC TGT CTC CCC GTG GCT CTC GGC CTA GCT GGG GCC CCA CAG ACC CCC
AGG ACA GAG GGG CAC CGA GAG CCG GAT CGA CCC CGG GGT GTC TGG GGG
Ser Cys Leu Pro Val Ala Leu Gly Leu Ala Gly Ala Pro Gln Thr Pro>
___a___a____TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a___a___a___>

680          690          700          710          720
  *      *     *      *      *     *      *      *     *      *
 GGC GTA GGT CGC GCA ATT TGG GTA AGG TCA TCG ATA CCC TTA CGT GCG
 CCG CAT CCA GCG CGT TAA ACC CAT TCC AGT AGC TAT GGG AAT GCA CGC
 Gly Val Gly Arg Ala Ile Trp Val Arg Ser Ser Ile Pro Leu Arg Ala>
 ___a___a____TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a___a___a___>

  730          740          750          760          770
    *      *     *      *      *     *      *      *     *
GCT TCG CCG ACC TCA TGG GGT ACA TAC CGC TCG TCG GCG CCC CTC TTG
CGA AGC GGC TGG AGT ACC CCA TGT ATG GCG AGC AGC CGC GGG GAG AAC
Ala Ser Pro Thr Ser Trp Gly Thr Tyr Arg Ser Ser Ala Pro Leu Leu>
___a___a____TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a___a___a___>
```

FIG. 12C

Substitute Figure

```
    780           790           800           810           820
*     *       *       *     *       *       *     *       *       *
GAG GCG CTG CCA GGG CCC TGG CGC ATG GCG TCC GGG TTC TGG AAG ACG
CTC CGC GAC GGT CCC GGG ACC GCG TAC CGC AGG CCC AAG ACC TTC TGC
Glu Ala Leu Pro Gly Pro Trp Arg Met Ala Ser Gly Phe Trp Lys Thr>
___a___a____TRANSLATION OF HCVSEND.SEQ (RITSA) [A]_a___a___a___>
```

```
       830           840
  *       *       *     *
 GCG TGA ACT ATG CAA CAG
 CGC ACT TGA TAC GTT GTC
 Ala *** Thr Met Gln Gln>
  ___TRANSLATION OF H____>
```

FIG. 12D

Substitute Figure

SEQUEBCE RANGE: 1 TO 166

```
         10          20          30          40          50          60
       *   *       *   *       *   *       *   *       *   *       *   *
*ARILNLKKK TNVTPTVAHR TSSSRVAVRS LVEFTCCRAG ALDWVCARRE RLPSGRNLEV

         70          80          90         100         110         120
     *   *       *   *       *   *       *   *       *   *       *   *
DVSLSPRLVG PRAGPGLSPG TLGPSMAMRA AGGRDGSCLP VALGLAGAPQ TPGVGRAIWV

        130         140         150         160
     *   *       *   *       *   *       *   *       *
RSSIPLRAAS PTSWGTYRSS APLLEALPGP WRMASGFWKT A*TMQQ
```

(SEQ ID NO:1)

FIG. 13

Substitute Figure